

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:17 ; Search time 170.72 Seconds  
(without alignments)  
17.102 Million cell updates/sec

Title: US-09-331-631A-1\_COPY\_74\_116  
Perfect score: 248  
Sequence: 1 NQEDPQTECQCQCRRCROE.....RQOQYCRCKEICEEYEE 43

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:\*

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	47.2	566	2 S22477	vicilin precursor
2	105	42.3	588	1 FWCNAB	alpha-globulin B p
3	104	41.9	509	2 S08059	alpha-globulin typ
4	96	38.7	411	2 S09475	hypothetical prote
5	94	37.9	605	2 S06398	alpha-globulin typ
6	80.5	32.5	425	2 T18592	hypothetical prote
7	80.5	32.5	600	2 T18593	hypothetical prote
8	80.5	32.5	572	2 T44430	protein PVI00 limp
9	79	31.9	520	2 T29880	hypothetical prote
10	78	31.5	47	2 JC5557	hypothetical prote
11	77.5	31.2	242	2 T29699	arginine/glutamate
12	74	29.8	388	2 T31887	hypothetical prote
13	74	29.8	388	2 T31888	hypothetical prote
14	74	29.8	438	2 T31889	hypothetical prote
15	74	29.8	445	2 T31898	hypothetical prote
16	73.5	29.6	335	2 T31560	hypothetical prote
17	73.5	29.6	335	2 T31561	hypothetical prote
18	72.5	29.2	330	2 T25169	hypothetical prote
19	71.5	28.8	335	2 T31559	hypothetical prote
20	70	28.2	1513	2 T23681	hypothetical prote
21	68.5	27.6	654	2 T30136	hypothetical prote
22	68	27.4	419	2 T18450	hypothetical prote
23	67	27.0	154	2 T27937	hypothetical prote
24	66.5	26.8	273	2 T20930	hypothetical prote
25	66.5	26.8	314	2 T27686	hypothetical prote
26	66.5	26.8	356	2 S31574	hypothetical prote
27	66.5	26.8	637	2 S35221	globulin begl prec
28	65	26.2	111	2 T20452	hypothetical prote
29	65	26.2	910	2 A34721	androgen receptor

30	65	26.2	911	2 B34721	androgen receptor
31	65	26.2	919	2 A39248	androgen receptor
32	65	26.2	1306	2 T13592	hypothetical prote
33	63.5	25.6	33	2 A41822	antimicrobial pept
34	63.5	25.6	51	1 HSMSS1	protamine 1 - mouse
35	63.5	25.6	51	2 S03997	protamine 1 - rat
36	62.5	25.2	342	2 JC7110	brain-specific mem
37	62	25.0	648	1 JQ1150	protein kinase (EC
38	61	24.6	1390	2 T14004	trif protein - sil
39	60	24.2	223	1 KASHS2	alpha-s2-casein pr
40	60	24.2	1969	2 T08875	histidine kinase h
41	60	24.2	4957	2 T03455	ALR protein - huma
42	60	24.2	5262	2 T03454	ALR protein - huma
43	59.5	24.0	294	2 T23682	hypothetical prote
44	59.5	24.0	1282	2 JF0120	glycoprotein A - m
45	59	23.8	285	1 I46207	involucrin - dog

## ALIGNMENTS

RESULT 1  
S22477  
vicilin precursor - cacao  
C:Species: Theobroma cacao (cacao)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C:Accession: S22477; S22478; S18105; S22050  
R:McHenry, L.; Fritz, P.J.  
Plant Mol. Biol. 18, 1173-1176, 1992  
A:Title: Comparison of the structure and nucleotide sequence of vicilin genes of coco  
A:Reference number: S22477; M0ID:9228309  
A:Accession: S22477  
A:Molecule type: DNA  
A:Residues: 1-566 <MCH>  
A:Cross-references: EMBL:X62625  
A:Accession: S22478  
A:Molecule type: mRNA  
A:Residues: 1-452 <MC2>  
A:Cross-references: EMBL:X62626  
C:Genetics:  
A:Introns: 211/1; 269/3; 296/3; 391/3; 502/1  
C:Superfamily: glycinin  
C:Keywords: seed; storage protein  
F:1-24/Domain: signal sequence #status predicted <Sig>  
F:25-566/Product: vicilin #status predicted <MNT>

Query Match 47.2%; Score 117; DB 2; Length 566;  
Best local similarity 50.0%; Pred. No. 4.2e-05;  
Matches: 20; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 2 QEDPQTECQCQCRRCROESGPRQOQYCRCKEICEEYEE 41  
Db 78 EEELQRYQOCQCRCEQDQGOGRQOQCRCKEYKEOE 117

RESULT 2  
FWCNAB  
alpha-globulin B precursor (clone C72) - upland cotton  
N:Alternate names: seed storage protein; vicilin precursor  
C:Species: Gossypium hirsutum (upland cotton)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.  
Plant Mol. Biol. 7, 475-489, 1986  
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII  
A:Reference number: A30838  
A:Accession: A30838  
A:Molecule type: mRNA  
A:Residues: 1-588 <CHL>  
A:Cross-references: GB:M16891; MID:q167374; PIDN:AAA33071.1; PID:q167375  
A:Experimental source: var. Coker 201  
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.





